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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/725,906	12/01/2003	Renu Wadhwa	14875-066002	5573

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EXAMINER	
BELYAVSKYI, MICHAIL A	

ART UNIT	PAPER NUMBER
1644	

DATE MAILED: 07/07/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/725,906	WADHWA ET AL.	
	Examiner	Art Unit	
	Michail A. Belyavskyi	1644	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *01 December 2003*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *8-11,13-20,22-25,28 and 34-46* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☒ Claim(s) *8-10,17-19,22-24,28,44 and 46* is/are allowed.

6)☒ Claim(s) *11,13-16,20,25,34-43 and 45* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *02/04/05;12/01/03*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

DETAILED ACTION

1. Applicant's amendment, filed 12/01/03 is acknowledged.

Claims 8-11, 13-20, 22-25, 28, 34-46 are pending and under consideration in the instant application.

2. The specification is objected to under 37 CFR 1.821(d) for failing to disclose SEQ ID NOS, for the amino acid sequence disclosed on page 18, line 2.

3. The specification on page 1, line 4 should be amended to reflect the status of the parent 09/684,579 application.

4. Acknowledgment is made of the claimed for foreign priority under 35 U.S.C. 119(a)-(d). Certified copy of foreign the priority document JP 10/115975 has been received in Application NO: 09/684,579.

5. The title of the invention is not descriptive. A new title is required that is clearly indicative of the invention *to which the claims are directed.*

6. The information disclosure statement filed 12/01/03 fails to comply with 37 CFR 1.98(a)(2), which requires a legible copy of each cited foreign patent document; each non-patent literature publication or that portion which caused it to be listed; and all other information or that portion which caused it to be listed. It has been placed in the application file, but the information referred to therein has not been considered.

7. The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

8. Claims 11, 13, 14, 15, 16, 20, 25 , 34-43 and 45 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for an isolated nucleic acid consisting of or comprising nucleotides 294 through 740 of SEQ ID NO:2, wherein said nucleic acid encodes a polypeptide of SEQ ID NO:1, or an isolated nucleic acid that encodes a polypeptide **consisting** of the amino acid sequence 76 through 149 of SEQ ID NO:1, or **consisting** of the amino acid sequence 1-75 of SEQ ID NO:1 wherein said polypeptide inhibits the differentiation of myoblasts into myotubes does not reasonably provide enablement for : (i) *Any* isolated nucleic acid comprising a strand that hybridized under high stringency condition to a single stranded probe, wherein said probe consists of nucleotides 294-through 740 of SEQ ID NO:2, or the complement thereof, wherein the nucleic acid encodes a polypeptide that inhibits the differentiation of myoblasts into myotubes, as claimed in claim 11, or (ii) wherein said polypeptide comprises SEQ ID NO:1, as claimed in claim 13; or (iii) wherein strand is at lest 15 nucleotides in length, as claimed in claim 14, or (iv) wherein the nucleic acid is an antisense nucleic acid that inhibits expression of a polypeptide comprising SEQ ID NO:1, as claimed in claim 15; or vector or a culture host cells comprising said nucleic acid as claimed in claims 20 and 25; or (v) *any* isolated nucleic acid encoding a polypeptide which comprises the amino acid sequence of SEQ ID NO:1 with 50, 30, or 10 conservative amino acid substitutions, as claimed in claims 34-36; or (vi) *any* isolated nucleic acid comprising a nucleotide sequence that is at least 70%, 90% or 95 % homologous to SEQ ID NO:2, as claimed in claims 37-39; or (vii) *any* isolated nucleic acid comprising a sequence that encodes a polypeptide which is 60%, 80% or 95 % identical to SEQ ID NO:1; or (viii) *any* isolated nucleic acid that encodes a polypeptide comprising the amino acid sequences of residues 76 to 149 of SEQ ID NO:1, as claimed in claim 43; or (ix) *any* isolated nucleic acid that encodes a polypeptide comprising the amino acid sequences of residues 1 through 75 of SEQ ID NO:1, as claimed in claims 45. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the invention commensurate in scope with these claims.

Factors to be considered in determining whether undue experimentation is required to practice the claimed invention are summarized *In re Wands* (858 F2d 731, 737, 8 USPQ2d 1400, 1404 (Fed. Cir. 1988)). The factors most relevant to this rejection are the scope of the claim, the amount of direction or guidance provided, the limited working examples, the unpredictability in the art and the amount of experimentation required to enable one of skill in the art to practice the claimed invention.

The claims as written encompass the genus of nucleic acid sequences . The genus encompasses nucleic acid sequences wherein such nucleic acid have numerous differences in nucleic acid sequences.

The Specification disclosed a discovery of a "striamin" polypeptide of SEQ ID NO:1, encoded by an nucleic acid consisting of or comprising nucleotides 294 through 740 of SEQ ID NO:2, wherein said polypeptide inhibits the differentiation of myoblasts into myotubes and can inhibit the activity of p53 (see entire document, pages 17 and overlapping pages 20-21 and Fig.1 in particular). The Specification explicitly disclosed that only the full length protein consisting of amino acid sequences 1-149 of SEQ ID NO:1, encoded by nucleotides 294 through 740 of SEQ ID NO:2; or polypeptide **consisting** of amino acid sequences of residues 76 through 149 of SEQ ID NO:1 can inhibits the differentiation of myoblasts into myotubes and can inhibit the activity of p53 (see Examples 8- 11 in particular).

Applicant has not taught how to make and/or use : (i) *Any* isolated nucleic acid comprising a strand that hybridized under high stringency condition to a single stranded probe, wherein said probe consists of nucleotides 294-through 740 of SEQ ID NO:2, or the complement thereof, wherein the nucleic acid encodes a polypeptide that inhibits the differentiation of myoblasts into myotubes, as claimed in claim 11, or (ii) wherein said polypeptide comprises SEQ ID NO:1, as claimed in claim 13; or (iii) wherein strand is at lest 15 nucleotides in length, as claimed in claim 14, or (iv) wherein the nucleic acid is an antisense nucleic acid that inhibits expression of a polypeptide comprising SEQ ID NO:1, as claimed in claim 15; or vector or a culture host cells comprising said nucleic acid as claimed in claims 20 and 25; or (v) *any* isolated nucleic acid encoding a polypeptide which comprises the amino acid sequence of SEQ ID NO:1 with 50, 30, or 10 conservative amino acid substitutions, as claimed in claims 34-36; or (vi) *any* isolated nucleic acid comprising a nucleotide sequence that is at least 70%, 90% or 95 % homologous to SEQ ID NO:2, as claimed in claims 37-39; or (vii) *any* isolated nucleic acid comprising a sequence that encodes a polypeptide which is 60%, 80% or 95 % identical to SEQ ID NO:1; or (viii) *any* isolated nucleic acid that encodes a polypeptide comprising the amino acid sequences of residues 76 to 149 of SEQ ID NO:1, as claimed in claim 43; or (ix) *any* isolated nucleic acid that encodes a polypeptide comprising the amino acid sequences of residues 1 through 75 of SEQ ID NO:1, as claimed in claims 45. The structural characteristics of said nucleic acid molecules are not defined in the claims.

Claim 11 recites an isolated nucleic acid comprising a strand that hybridized under high stringency condition to a single stranded probe, wherein said probe consists of nucleotides 294-through 740 of SEQ ID NO:2, or the complement thereof, wherein the nucleic acid encodes a polypeptide that inhibits the differentiation of myoblasts into myotubes. The claim as written reads on antisense nucleic acid. The translation of said complementary (antisense) nucleic acid sequence does not encode the "striamin" polypeptide of SEQ ID NO:1. In addition, claims 14 and 16 both reads on a nucleic acid of at least 15 nucleic acid that encodes a polypeptide that inhibits the differentiation of myoblasts in to myotubes. The polypeptide encoded by said nucleic acids would comprise of at least 5 amino acid. The Specification however, does not

provide sufficient guidance with regards to what is the minimum length , structure and composition that is required for a polypeptide to maintaining the same function as of "striamin" polypeptide of SEQ ID NO:1.

In addition, the fact that two nucleic acid sequences will hybridize under stringent conditions does not in and of itself require that the two sequences share any functional activity. Thus, the same observations apply to the recitation of "isolated nucleic acid comprising a strand that hybridized under high stringency condition to a single stranded probe, wherein said probe consists of nucleotides 294-through 740 of SEQ ID NO:2, or the complement thereof, wherein the nucleic acid encodes a polypeptide that inhibits the differentiation of myoblasts into myotubes. It was well known in the art at the time the invention was made that hybridization could occur between two sequence based upon short stretches of 100% identity. Thus a great deal of sequence variability *with respect to the full-length nucleic acid* is possible and in the absence of a clear recitation that the identity is over nucleotides 294-through 740 of SEQ ID NO:2, the claim reads on subsequences and would be viewed by the skilled artisan as been even less likely to encode a polypeptide with the same function as polypeptide encoded by SEQ ID NO:1. Thus, as for the recitation of percent identity, hybridization language in the absence limitations regarding the *sequence length over which the hybridization takes place*; does not allow the skilled artisan to make and use the hybridizing nucleic acids commensurate in scope with the instant claims without undue experimentation.

Finally, the use of antisense nucleic acid to inhibit expression of a polypeptide comprising SEQ ID NO:1as claimed in claim 15 is well known in the art to be highly unpredictable, even though the level of skill in the art is high. For instance, Mountain reviews in TIBTECH (18:119-128 2000) that while much progress has been made in the field of gene therapy, developing effective gene therapies is much more demanding than originally anticipated (e.g., pg 120, middle); and that most of the difficulty lies with the development of effective vectors since the vectors in use all have both advantages and disadvantages (e.g., Table 4). Mountain concludes that it is unlikely that a universal vector will emerge in the next few years (page 125, middle of 1st column). Similarly, although antisense therapy has progressed in recent years, there is still a high level of unpredictability in the art. This unpredictability was summarized recently by Branch (TIBS 1998; 23:45-50). In particular, difficulties in ensuring that the oligo interacts with its single gene target versus other genes, and a variety of unexpected non-antisense effects, complicate the use of antisense compounds (e.g., summarized in Abstract). It is noted that specification as filed does not provide any examples of the nucleic acids that inhibits the expression of a polypeptide comprising SEQ ID NO:1. Thus in the absence of working examples or detailed guidance in the specification, the intended uses of any pharmaceutical composition comprising an antisense nucleic acid are fraught with uncertainties.

The instant claims encompass in their breadth *any* nucleic acid encoding a polypeptide "with at least about 60%, 80% or 95% identity to SEQ ID NO:1"; or *any* nucleic acid that "encoding a polypeptide with 50, 30 or 10 conservative amino acid substitutions".

There does not appear to be sufficient guidance in the specification as filed as to how the skilled artisan would make and use the various nucleic acids recited in the instant claims. A person of skill in the art would not know which sequences are essential, which sequences are non-essential, and what particular sequence lengths identify essential sequences. There is insufficient guidance to direct a person of skill in the art to select particular sequences or sequence lengths as essential for inhibiting the differentiation of myoblasts into myotubes . Without detailed direction as to which nucleic acid sequences are essential to the function of the encoded polypeptide, a person of skill in the art would not be able to determine without undue experimentation which of the plethora of nucleic acid sequences encompassed by the instant claims would share the ability to inhibit the differentiation of myoblasts into myotubes other than an isolated nucleic acid consisting of or comprising nucleotides 294 through 740 of SEQ ID NO:2, wherein said nucleic acid encodes a polypeptide of SEQ ID NO:1, or an isolated nucleic acid that encodes a polypeptide **consisting** of the amino acid sequence 76 through 149 of SEQ ID NO:1. Wadhwa et al., (J of Biol. Sci. 1999, 274, pages 14948 – 14955) teach that *Striamin* protein does not share any structural homology to any proteins known to be involved to any aspects of muscle differentiation and only very specific sequences of said protein are capable of repressing transcriptional activity of p53 and that characterization of the sequences essential for *Striamin* protein function has yet to be done (see entire document, page 14954 in particular).

Attwood (Science 2000; 290:471-473) teaches that "[i]t is presumptuous to make functional assignments merely on the basis of some degree of similarity between sequences. Similarly, Skolnick et al. (Trends in Biotech. 2000; 18(1):34-39) teach that the skilled artisan is well aware that assigning functional activities for any particular protein or protein family based upon sequence homology is inaccurate, in part because of the multifunctional nature of proteins (e.g., "Abstract" and "Sequence-based approaches to function prediction", page 34). Even in situations where there is some confidence of a similar overall structure between two proteins, only experimental research can confirm the artisan's best guess as to the function of the structurally related protein (see in particular "Abstract" and Box 2). Finally, even single amino acid differences can result in drastically altered functions between two proteins. For example, Metzler et al. (Nature Structural Biol. 1997; 4:527-531) show that any of a variety of single amino acid changes can alter or abolish the ability of CTLA4 to interact with its ligands CD80 and CD86 (e.g., summarized in Table 2). Burgess et al (J Cell Biol. 111:2129-2138, 1990) show that a conservative replacement of a single "lysine" reside at position 118 of acidic fibroblast growth factor by "glutamic acid" led to the substantial loss of heparin binding, receptor binding and biological activity of the protein. Similarly, Lazar et al. (Mol Cell Biol. 8:1247-1252, 1988) teach that in transforming growth factor alpha, replacement of aspartic acid at position 47 with alanine or asparagines did not affect biological activity while replacement with serine or glutamic acid sharply reduced the biological activity of the mitogen. These references demonstrate that even a single amino acid substitution or what appears to be an inconsequential chemical modification will often dramatically affect the biological activity and characteristic of a protein. Furthermore, the specification fails to teach what deletions, truncations, substitutions and mutations of the disclosed sequence can be tolerated that will allow the protein to function as claimed. While it is known that many amino acid substitutions are possible in any given protein, the position within the protein's sequence where such amino acid substitutions can be made with

reasonable expectation of success are limited. Certain positions in the sequence are critical to the three-dimensional structure/function relationship, and these regions can tolerate only conservative substitutions or no substitutions. Residues that are directly involved in protein functions such as binding will certainly be among the most conserved (Bowie et al. Science, 247:1306-1310, 1990).

Since the nucleic acid sequence of a polynucleotide determines its protein coding properties, predictability of which changes can be tolerated in a polynucleotide's nucleic acid sequence and still retain similar functions and properties requires a knowledge of, and guidance with regard to which nucleic acids within the full-length nucleotide sequence, if any, are tolerant of modification and which are conserved or less tolerant to modification, and detailed knowledge of the ways in which the product's structure relates to its functional usefulness. Because there is no guidance in the specification as to which amino acid sequence within the full-length amino acid sequence of SEQ ID NO: 1, which encoded *Striamin* protein that after substitution, deletion or insertion will retain the same function, it is unpredictable to determine which polynucleotide comprising a polynucleotide sequence that encodes a polynucleotide sequence that has at least about 60%, 80% or 95% identity to SEQ ID NO:1"; or *any* nucleic acid that "encoding a polypeptide with 50, 30 or 10 conservative amino acid substitutions will have similar function. Since the structure associated with functions of any polynucleotide mentioned above are not disclosed, predicting which polynucleotide that about 60%, 80% or 95% identity to SEQ ID NO:1"; or *any* nucleic acid that "encoding a polypeptide with 50, 30 or 10 conservative amino acid substitutions" having the same function as amino acid sequence of SEQ ID NO: 1 is well outside the realm of routine experimentation.

Thus it is unpredictable if any functional activity will be shared by two polypeptides having less than 100% identity over the full length of their sequences. In view of this unpredictability; the skilled artisan would not reasonably expect a polypeptide having anything less than 100% identity *over the full length of SEQ ID NO:1* to *share the same function* as the polypeptide of SEQ ID NO:1. Thus the recitation of percent identity language, in the absence of limitations regarding the *sequence length over which the percent identity is required*; does not allow the skilled artisan to make and use the encoding nucleic acids commensurate in scope with the instant claims without undue experimentation.

Also an issue is that "comprising" is considered open-ended claim language and expand an isolated nucleic acid molecule to include additional non disclosed nucleic acids sequences outside of the specified sequences. It means that a peptide may include additional unrecited amino acid on either or both of the N or C-terminus of a given sequence. The disclosure of polypeptide of SEQ ID NO:1, encoded by an nucleic acid consisting of nucleotides 294 through 740 of SEQ ID NO:2, wherein said polypeptide inhibits the differentiation of myoblasts into myotubes and can inhibit the activity of p53 cannot support the entire genus of: *any* isolated nucleic acid that encodes a polypeptide comprising the amino acid sequences of residues 76 to 149 of SEQ ID NO:1, as claimed in claim 43; or *any* isolated nucleic acid that encodes a polypeptide comprising the amino acid sequences of residues 1 through 75 of SEQ ID NO:1, as

claimed in claims 45 as part of their sequence. Applicant is relying upon certain biological activities and the disclosure of a single species to support an entire genus. As has been discussed supra, minor structural differences among even structurally related compounds or compositions can result in substantially different biology, expression, and pharmacology of proteins. Therefore, structurally unrelated *any* isolated nucleic acid that encodes a polypeptide comprising the amino acid sequences of residues 76 to 149 of SEQ ID NO:1, as claimed in claim 43; or *any* isolated nucleic acid that encodes a polypeptide comprising the amino acid sequences of residues 1 through 75 of SEQ ID NO:1, as claimed in claims 45 as part of their sequence encompassed by the claimed invention would be expected to have greater differences in their activities.

Since the instant fact pattern fails to indicate that representative number of structurally related compounds is disclosed, the artisan would not know the identity of a reasonable number of representative compounds falling within the scope of the instant claims and consequently would not know how to make them. An assay for *finding* a product is not equivalent to a positive recitation of *how to make* a product.

Thus, Applicant has not provided sufficient guidance to enable one skill in the art to make and use claimed (i) *Any* isolated nucleic acid comprising a strand that hybridized under high stringency condition to a single stranded probe, wherein said probe consists of nucleotides 294-through 740 of SEQ ID NO:2, or the complement thereof, wherein the nucleic acid encodes a polypeptide that inhibits the differentiation of myoblasts into myotubes, as claimed in claim 11, or (ii) wherein said polypeptide comprises SEQ ID NO:1, as claimed in claim 13; or (iii) wherein strand is at lest 15 nucleotides in length, as claimed in claim 14, or (iv) wherein the nucleic acid is an antisense nucleic acid that inhibits expression of a polypeptide comprising SEQ ID NO:1, as claimed in claim 15; or vector or a culture host cells comprising said nucleic acid as claimed in claims 20 and 25; or (v) *any* isolated nucleic acid encoding a polypeptide which comprises the amino acid sequence of SEQ ID NO:1 with 50, 30, or 10 conservative amino acid substitutions, as claimed in claims 34-36; or (vi) *any* isolated nucleic acid comprising a nucleotide sequence that is at least 70%, 90% or 95 % homologous to SEQ ID NO:2, as claimed in claims.37-39; or (vii) *any* isolated nucleic acid comprising a sequence that encodes a polypeptide which is 60%, 80% or 95 % identical to SEQ ID NO:1; or (viii) *any* isolated nucleic acid that encodes a polypeptide comprising the amino acid sequences of residues 76 to 149 of SEQ ID NO:1, as claimed in claim 43; or (ix) *any* isolated nucleic acid that encodes a polypeptide comprising the amino acid sequences of residues 1 through 75 of SEQ ID NO:1, as claimed in claims 45. in a manner reasonably correlated with the scope of the claims. The scope of the claims must bear a reasonable correlation with the scope of enablement. *In re Fisher*, 166 USPQ 18 (CCPA 1970) indicates that the more unpredictable an area is, the more specific enablement is necessary in order to satisfy the statute.

In view of the quantity of experimentation necessary, the unpredictability of the art, the lack of sufficient guidance in the specification, the limited working examples, and the limited amount of direction provided given the breadth of the claims, it would take undue trials and errors to practice the claimed invention.

9. Claims 43 and 45 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Applicant is in possession of : an isolated nucleic acid consisting of or comprising nucleotides 294 through 740 of SEQ ID NO:2, wherein said nucleic acid encodes a polypeptide of SEQ ID NO:1, or an isolated nucleic acid that encodes a polypeptide **consisting** of the amino acid sequence 76 through 149 of SEQ ID NO:1, or **consisting** of the amino acid sequence 1-75 of SEQ ID NO:1 wherein said polypeptide inhibits the differentiation of myoblasts into myotubes

Applicant is not in possession of : (i) *any* isolated nucleic acid that encodes a polypeptide comprising the amino acid sequences of residues 76 to 149 of SEQ ID NO:1, as claimed in claim 43; or (ii) *any* isolated nucleic acid that encodes a polypeptide comprising the amino acid sequences of residues 1 through 75 of SEQ ID NO:1, as claimed in claims 45.

The claimed invention is drawn to a genus of nucleic acid sequences . The genus encompasses nucleic acid sequences wherein such nucleic acid have numerous differences in nucleic acid sequences. However, the structural identifying characteristics of the genus are not disclosed. There is no evidence that there is any *per se* structure/function relationship between the disclosed isolated nucleic acid consisting of or comprising nucleotides 294 through 740 of SEQ ID NO:2, wherein said nucleic acid encodes a polypeptide of SEQ ID NO:1 that inhibits the differentiation of myoblasts in to myotubes and claimed : (i) *any* isolated nucleic acid that encodes a polypeptide comprising the amino acid sequences of residues 76 to 149 of SEQ ID NO:1, as claimed in claim 43; or (ii) *any* isolated nucleic acid that encodes a polypeptide comprising the amino acid sequences of residues 1 through 75 of SEQ ID NO:1, as claimed in claims 45.
Applicant has disclosed a limited number of species; therefore, the skilled artisan cannot envision all the contemplated amino acid sequence possibilities recited in the instant claims. Consequently, conception in either case cannot be achieved until a representative description of the structural and functional properties of the claimed invention has occurred, regardless of the complexity or simplicity of the method. Adequate written description requires more than a mere statement that it is part of the invention. The sequences themselves are required. See Fiers v. Revel, 25 USPQ2d 1601, 1606 (CAFC 1993).

A description of nucleic acid sequences by functional language in the absence of a structure is not considered sufficient to show possession of the claimed invention. A description of what a material does rather than of what it is, usually does not suffice. See Fiers, 984 F.2d at 1169-71, 25 USPQ2D at 1605-06. It is only a definition of a useful result rather than a definition of what achieves that result. Many species may achieve that result. The definition requirement of the patent statute requires a description of an invention, not an indication of a result that one might

achieve if one made that invention. See *In re Wilder*, 736 /f.2d 1516, 1521, 22 USPQ 369, 372-73 (Fed. Cir. 1984) affirming the rejection because the specification does "little more than outline[e] goals appellants hope the claimed invention achieves and the problems the invention will hopefully ameliorate.") Accordingly, naming a type of material generally known to exist, in the absence of knowledge as to what the material consists of (e.g. structural feature), is not a description of that material.

A description of a genus of nucleic acid sequences may be achieved by means of a recitation of a representative number of polypeptide sequences, defined by amino acid sequence, falling within the scope of the genus, or of a recitation of structural features common to the genus, which features constitute a substantial portion of the genus. Regents of the University of California v. Eli Lilly&Co., 119F3d 1559, 1569, 43 USPQ2d 1398, 1406 (Fed. Cir. 1997).

Vas-Cath Inc. v. Mahurkar, 19 USPQ2d 1111, makes clear that "applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession of the invention. The invention is, for purposes of the written description inquiry, whatever is now claimed." (See page 1117.) The specification does not "clearly allow persons of ordinary skill in the art to recognize that [he or she] invented what is claimed." (See Vas-Cath at page 1116.). Consequently, Applicant was not in possession of the instant claimed invention. See University of California v. Eli Lilly and Co. 43 USPQ2d 1398.

Applicant is directed to the Guidelines for the Examination of Patent Applications Under the 35 U.S.C. 112, ¶ 1 "Written Description" Requirement, Federal Register, Vol. 66, No. 4, pages 1099-1111, Friday January 5, 2001.

10. It is noted that US Patent 6,458,533 teach an 60 mer probe comprising 17 nucleotides (SEQ ID NO:95) that are 100% identical to nucleotides 541-557 of SEQ ID NO:2. However, said reference is not a prior art reference since US Patent '533 does not teach that said probe encodes a polypeptide that inhibits the differentiation of myoblasts into myotubes.

11. The prior art does not teach or suggest the claim invention recited in claims 8-10, 17-19, 22-24, 28, 44 and 46.

12. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Michail Belyavskyi whose telephone number is 571/272-0840. The examiner can normally be reached Monday through Friday from 9:00 AM to 5:30 PM. A message may be left on the examiner's voice mail service. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Christina Chan can be reached on 571/272-0841.

The fax number for the organization where this application or proceeding is assigned is 571/273-8300

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

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June 27, 2005